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46

RAW SEQUENCE LISTING PATENT APPLICATION US/09/001,039A

DATE: 08/06/98 TIME: 12:40:51

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This Raw Listing contains the General Information Section and up to the first 5 pages.

```
1
                                       SEQUENCE LISTING
                                                                ENTERED
     (1)
            General Information:
 5
          (i) APPLICANT: Chiron Corporation
 6
 7
         (ii) TITLE OF INVENTION: Methods for Administration of
            Recombinant Gene Delivery Vehicles for Treatment of Hemophilia
 8
 9
            and Other Disorders
10
11
        (iii) NUMBER OF SEQUENCES: 83
12
         (iv) CORRESPONDENCE ADDRESS:
13
14
               (A) ADDRESSEE: Chiron Corporation
15
               (B) STREET: 4560 Horton Street
               (C) CITY: Emeryville
16
17
               (D) STATE: California
18
               (E) COUNTRY: U.S.A.
19
               (F) ZIP: 94608
20
21
          (v) COMPUTER READABLE FORM:
               (A) MEDIUM TYPE: Floppy disk
23
               (B) COMPUTER: IBM PC compatible
24
               (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25
               (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
26
27
         (vi) CURRENT APPLICATION DATA:
28
               (A) APPLICATION NUMBER:
29
               (B) FILING DATE:
30
               (C) CLASSIFICATION:
31
32
      (Viii) ATTORNEY/AGENT INFORMATION:
33
               (A) NAME: Kruse, Norman J.
34
               (B) REGISTRATION NUMBER: 35,235
35
               (C) REFERENCE/DOCKET NUMBER: 1155.005
36
37
         (ix) TELECOMMUNICATION INFORMATION:
38
               (A) TELEPHONE: (510) 923-3520
39
               (B) TELEFAX: (510) 655-3542
40
41
42
43
    (2) INFORMATION FOR SEQ ID NO:1:
44
         (i) SEQUENCE CHARACTERISTICS:
45
               (A) LENGTH: 24 base pairs
```

(B) TYPE: nucleic acid

RAW SEQUENCE LISTING PATENT APPLICATION US/09/001,039A

DATE: 08/06/98 TIME: 12:40:52

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47	(C) STRANDEDNESS: single	
48	(D) TOPOLOGY: linear	
49	(ii) MOLECULE TYPE: DNA (genomic)	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:	
51	GAGAGATGGG GGAGGCTAAC TGAG	24
52		
53	(2) INFORMATION FOR SEQ ID NO:2:	
54	(i) SEQUENCE CHARACTERISTICS:	
55	(A) LENGTH: 28 base pairs	
56	(B) TYPE: nucleic acid	
57	(C) STRANDEDNESS: single	
58	(D) TOPOLOGY: linear	
59	(ii) MOLECULE TYPE: DNA (genomic)	
60	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:	
61	GATCCTCAGT TAGCCTCCCC CATCTCTC	28
62		
63	(2) INFORMATION FOR SEQ ID NO:3:	
64	(i) SEQUENCE CHARACTERISTICS:	
65	(A) LENGTH: 35 base pairs	
66	(B) TYPE: nucleic acid	
67	(C) STRANDEDNESS: single	
68	(D) TOPOLOGY: linear	
69	<pre>(ii) MOLECULE TYPE: DNA (genomic)</pre>	
70	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:	
71	TATATCTCCA GATGAGGTAC ATGATTTTAG GCTTG	35
72		
73	(2) INFORMATION FOR SEQ ID NO:4:	
74	(i) SEQUENCE CHARACTERISTICS:	
75	(A) LENGTH: 40 base pairs	
76	(B) TYPE: nucleic acid	
77	(C) STRANDEDNESS: single	
78	(D) TOPOLOGY: linear	
79	(ii) MOLECULE TYPE: DNA (genomic)	
80	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:	
81	TATATATCGA TTCAAGGCAT TTTCTTTTCA TCAATAAAAC	40
82	(A) INDADVINTAN DAD GDA ID NA -	
83	(2) INFORMATION FOR SEQ ID NO:5:	
84 85	(i) SEQUENCE CHARACTERISTICS:	
86	(A) LENGTH: 37 base pairs	
	(B) TYPE: nucleic acid	
87	(C) STRANDEDNESS: single	
88 89	(D) TOPOLOGY: linear	
90	(ii) MOLECULE TYPE: DNA (genomic)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:	
91 92	TCGAGGATCC GCCCGGGCGG CCGCATCGAT GTCGACG	37
93	(2) INFORMATION FOR SEC ID NO. (.	
94	(2) INFORMATION FOR SEQ ID NO:6: (i) SEQUENCE CHARACTERISTICS:	
95	(1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 35 base pairs	
96	(B) TYPE: nucleic acid	
90 97	(B) TYPE: NUCLEIC acid (C) STRANDEDNESS: single	
98		
99	(D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic)	
22	(II) MOLECOLE IIPE: DNA (genomic)	

RAW SEQUENCE LISTING PATENT APPLICATION US/09/001,039A

DATE: 08/06/98 TIME: 12:40:53

INPUT SET: S27916.raw

100	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:	
101	CGCGTCGACA TCGATGCGGC CGCCCGGGCG GATCC	35
102		
103		
104	(2) INFORMATION FOR SEQ ID NO:7:	
105	(i) SEQUENCE CHARACTERISTICS:	
106	(A) LENGTH: 77 base pairs	•
107	(B) TYPE: nucleic acid	
108	(C) STRANDEDNESS: single	
109	(D) TOPOLOGY: linear	
110	(ii) MOLECULE TYPE: DNA (genomic)	
111	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:	
112	AGTGAATTCG AGCTCGGTAC CCGGGGATCC TCTAGAGTCG ACCTGCAGGC ATGCAAGCTT	60
113	GCCTAATCA TGGTCAT	60
114	GCGTARICA IGGICAI	77
115	(2) INCODVACTON FOR CEO ID NO. 0.	
116	(2) INFORMATION FOR SEQ ID NO:8:	
117	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 8 amino acids	
118	(B) TYPE: amino acid	
119	(C) STRANDEDNESS: single	
120	(D) TOPOLOGY: linear	
121	(ii) MOLECULE TYPE: protein	
122	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:	
123	Ala Arg Glu Met Gly Glu Ala Asn	
124	1 5	
125		
126	(2) INFORMATION FOR SEQ ID NO:9:	
127	(i) SEQUENCE CHARACTERISTICS:	
128	(A) LENGTH: 27 base pairs	
129	(B) TYPE: nucleic acid	
130	(C) STRANDEDNESS: single	
131	(D) TOPOLOGY: linear	
132	(ii) MOLECULE TYPE: DNA (genomic)	
133	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:	
134	CCCGAGAGAT GGGGGAGGCT AACTGAG	27
135		
136	(2) INFORMATION FOR SEQ ID NO:10:	
137	(i) SEQUENCE CHARACTERISTICS:	
138	(A) LENGTH: 31 base pairs	
139	(B) TYPE: nucleic acid	
140	(C) STRANDEDNESS: single	
141	(D) TOPOLOGY: linear	
142	(ii) MOLECULE TYPE: DNA (genomic)	
143	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:	
144	GGGCTCTCTA CCCCCTCCGA TTGACACCTA G	31
145		
146	(2) INFORMATION FOR SEQ ID NO:11:	
147	(i) SEQUENCE CHARACTERISTICS:	
148	(A) LENGTH: 5 amino acids	
149	(B) TYPE: amino acid	
150	(C) STRANDEDNESS: single	
151	(D) TOPOLOGY: linear	
152	(ii) MOLECULE TYPE: protein	

RAW SEQUENCE LISTING PATENT APPLICATION US/09/001,039A

DATE: 08/06/98 TIME: 12:40:54

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153	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:	
154	Thr Ile Met Thr Met	
155	1 5	
156		
157		
158	(2) INFORMATION FOR SEQ ID NO:12:	
	· ·	
159	(i) SEQUENCE CHARACTERISTICS:	
160	(A) LENGTH: 24 base pairs	
161	(B) TYPE: nucleic acid	
162	(C) STRANDEDNESS: single	
163	(D) TOPOLOGY: linear	
164	(ii) MOLECULE TYPE: DNA (genomic)	
165	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:	
166	CCCTGTGCCT TATTTGAACT AACC	24
167		
168	(2) INFORMATION FOR SEQ ID NO:13:	
169	(i) SEQUENCE CHARACTERISTICS:	
170	(A) LENGTH: 24 base pairs	
	(B) TYPE: nucleic acid	
171		
172	(C) STRANDEDNESS: single	
173	(D) TOPOLOGY: linear	
174	(ii) MOLECULE TYPE: DNA (genomic)	
175	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:	
176	CCCACCACAA CCACATATCC CTCC	24
177		
178	(2) INFORMATION FOR SEQ ID NO:14:	
179	(i) SEQUENCE CHARACTERISTICS:	
180	(A) LENGTH: 19 base pairs	
181	(B) TYPE: nucleic acid	
182	(C) STRANDEDNESS: single	
183	(D) TOPOLOGY: linear	
184	(ii) MOLECULE TYPE: DNA (genomic)	
185	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:	19
186	CCAGTCCTCC GATTGACTG	19
187		
188	(2) INFORMATION FOR SEQ ID NO:15:	
189	(i) SEQUENCE CHARACTERISTICS:	
190	(A) LENGTH: 8332 base pairs	
191	(B) TYPE: nucleic acid	
192	(C) STRANDEDNESS: single	
193	(D) TOPOLOGY: linear	
194	(ii) MOLECULE TYPE: DNA (genomic)	
195	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:	
196	(,	
197	GCGCCAGTCC TCCGATTGAC TGAGTCGCCC GGGTACCCGT GTATCCAATA AACCCTCTTG	60
198	Controlled Total Total Controlled	
199	CAGTTGCATC CGACTTGTGG TCTCGCTGTT CCTTGGGAGG GTCTCCTCTG AGTGATTGAC	120
	CAGIIGORIC CORCITOIGG ICICGCIGII CCIIGGGRGG GICICCICIG RGIGRIIGRC	120
200	maggamaaa aaaaaamamm maammmaaaa aamaamaaaa aamaadaaaa aacamaaaaa	100
201	TACCCGTCAG CGGGGGTCTT TCATTTGGGG GCTCGTCCGG GATCGGGAGA CCCCTGCCCA	180
202		0.4.0
203	GGGACCACCG ACCCACCACC GGGAGGTAAG CTGGCCAGCA ACTTATCTGT GTCTGTCCGA	240
204		
205	TTGTCTAGTG TCTATGACTG ATTTTATGCG CCTGCGTCGG TACTAGTTAG CTAACTAGCT	300

PAGE: 5

RAW SEQUENCE LISTING PATENT APPLICATION US/09/001,039A

DATE: 08/06/98 TIME: 12:40:54

INPUT SET: S27916.raw

					4	MEUL SEL. 32/	710.14W
206 207 208	CTGTATCTGG	CGGACCCGTG	GTGGAACTGA	CGAGTTCGGA	ACACCCGGCC	GCAACCCTGG	360
208 209 210	GAGACGTCCC	AGGGACTTCG	GGGGCCGTTT	TTGTGGCCCG	ACCTGAGTCC	AAAAATCCCG	420
211 212	ATCGTTTTGG	ACTCTTTGGT	GCACCCCCCT	TAGAGGAGGG	ATATGTGGTT	CTGGTAGGAG	480
213 214	ACGAGAACCT	AAAACAGTTC	CCGCCTCCGT	CTGAATTTTT	GCTTTCGGTT	TGGGACCGAA	540
215 216	GCCGCGCCGC	GCGTCTTGTC	TGCTGCAGCA	TCGTTCTGTG	TTGTCTCTGT	CTGACTGTGT	600
217 218	TTCTGTATTT	GTCTGAGAAT	ATGGGCCAGA	CTGTTACCAC	TCCCTTAAGT	TTGACCTTAG	660
219 220	GTCACTGGAA	AGATGTCGAG	CGGATCGCTC	ACAACCAGTC	GGTAGATGTC	AAGAAGAGAC	720
221 222	GTTGGGTTAC	CTTCTGCTCT	GCAGAATGGC	CAACCTTTAA	CGTCGGATGG	CCGCGAGACG	780
223 224	GCACCTTTAA	CCGAGACCTC	ATCACCCAGG	TTAAGATCAA	GGTCTTTTCA	CCTGGCCCGC	840
225 226	ATGGACACCC	AGACCAGGTC	CCCTACATCG	TGACCTGGGA	AGCCTTGGCT	TTTGACCCCC	900
227 228	CTCCCTGGGT	CAAGCCCTTT	GTACACCCTA	AGCCTCCGCC	TCCTCTTCCT	CCATCCGCCC	960
229 230	CGTCTCTCCC	CCTTGAACCT	CCTCGTTCGA	CCCCGCCTCG	ATCCTCCCTT	TATCCAGCCC	1020
231 232	TCACTCCTTC	TCTAGGCGCC	AAACCTAAAC	CTCAAGTTCT	TTCTGACAGT	GGGGGGCCGC	1080
233 234	TCATCGACCT	ACTTACAGAA	GACCCCCCGC	CTTATAGGGA	CCCAAGACCA	CCCCCTTCCG	1140
235 236	ACAGGGACGG	AAATGGTGGA	GAAGCGACCC	CTGCGGGAGA	GGCACCGGAC	CCCTCCCCAA	1200
237 238				CCCCTGTGGC			1260
239 240	CATTCCCCCT	CCGCGCAGGA	GGAAACGGAC	AGCTTCAATA	CTGGCCGTTC	TCCTCTTCTG	1320
241 242	ACCTTTACAA	CTGGAAAAAT	AATAACCCTT	CTTTTTCTGA	AGATCCAGGT	AAACTGACAG	1380
243 244				AGCCCACCTG			1440
245 246	TGGGGACTCT	GCTGACCGGA	GAAGAAAAC	AACGGGTGCT	CTTAGAGGCT	AGAAAGGCGG	1500
247 248		•		TGCCCAATGA			1560
2 4 9 250				AGGCAGGTAG			1620
251 252				CGGGCAGAAG			1680
253 254				CTCCCTCGGC			1740
255 256				CTGAGGACCC			1800
257 258	CTATGTCTTT	CATTTGGCAG	TCTGCCCCAG	ACATTGGGAG	AAAGTTAGAG	AGGTTAGAAG	1860

PAGE: 1

SEQUENCE VERIFICATION REPORT PATENT APPLICATION *US/09/001,039A*

DATE: 08/06/98 TIME: 12:40:55

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